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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: Application of DEBINSKI, et al.

Application No.:	10/053,406	Examiner:	Andres, J.
Date filed:	January 17, 2002	Group:	1646

For: NUCLEIC ACIDS ENCODING IL 13 MUTANTS

CERTIFICATE UNDER 37 CFR 1.8(a)
I hereby certify that this correspondence is being deposited with the U.S. Postal Service as First Class mail in an envelope addressed to Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on May 15, 2003.
Reg. No. 42,730
Stanley A. Kim, Ph.D., Esq.

RESPONSE

Mail Stop Fee Amendment
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

In the office action mailed March 25, 2003 (the "Office Action"), the examiner indicated that the application contains claims directed to the following allegedly distinct species: the polynucleotides of SEQ ID NOs: 2-23. The Office Action required election of only one of the alleged species for further prosecution.

In response, if no generic claim is held allowable, the species wherein the purified nucleic acid encodes a polypeptide having or consisting of the amino acid sequence of SEQ ID NO: 2 is provisionally elected with traverse. Claims 1 and 24 are generic to the elected species.

The species election requirement is improper for a few reasons. First, 37 C.F.R. 1.141 states "[t]wo or more independent and distinct inventions may not be claimed in one national application, except that more than one species of an invention, not to exceed a reasonable number, may be specifically claimed in different claims in one national application, provided the

application also includes an allowable claim generic to all the claimed species and all the claims to species in excess of one are written in dependent form or otherwise include all the limitations of the generic claim." The twenty-two claimed species (i.e., the nucleic acid encoding the polypeptides of SEQ ID NOs: 2-23) do not exceed a reasonable number. Second, the nucleic acids at issue encode proteins that share common features. Namely, the proteins encoded are all multiple amino acid substitution mutants of hIL13. All contain alpha-helical core topology, consisting of four alpha helical regions (helices A, B, C and D) arranged in a "bundled core." Additionally, the nucleic acids encoding the proteins may be cloned using amplification methods involving a common substrate. Such an amplification method is one in which the gene for native hIL13 is PCR-amplified using primers that introduce the mutations. Moreover, all species encode proteins sharing a common functionality, e.g., analyzing the function of IL13 receptors. Third, as each of the different species is closely related to the others in sequence, a search for similar sequences would not be unduly burdensome.

Accordingly, reconsideration and withdrawal of the outstanding species election requirement is respectfully requested.

Respectfully submitted,

Dated: May 15, 2003

Stanley A. Kim, Ph.D., Esq.
Registration No. 42,730
AKERMAN SENTERFITT
222 Lakeview Avenue, Suite 400
West Palm Beach, FL 33402-3188
Tel: 561-653-5000